be found throughout the specification as originally filed, particularly at p. 15, line 20 to p. 16, line 2.

Applicants have amended claim 20 in order to recite the claim in independent form. Support for this amendment may be found, e.g., in claim 20 as originally filed.

Applicants have amended claims 22-24 to improve their form. Applicants have amended the claim dependency of claim 22, and have amended claims 23 and 24 for clarity. Support for these amendments may be found, e.g., in claims 22-24 as originally filed.

None of these amendments add new matter.

The Objections

37 C.F.R. 1.75(c)

The Examiner has objected to claim 20 as being in improper dependent form for failing to further limit the subject matter of a previous claim. Specifically, the Examiner contends that claim 20 recites a set of structure coordinates that is broader in scope than parent claim 19. The Examiner states that applicants are required to cancel the claim, amend the claim, or rewrite the claim in independent form. Applicants have rewritten claim 20 in independent form, thus obviating this objection.

The Rejections

35 U.S.C. § 101

Claims 19-24 stand rejected under 35 U.S.C. § 101 as being directed to non-statutory subject matter. Specifically, the Examiner contends that independent claims 19 and 21 recite mathematical operations and do not recite any concrete or tangible results and are thus non-statutory. In light of the claim amendments, applicants traverse.

Applicants' amended claims 19 and 21 recite the additional step of "outputting said quantified association to a suitable output hardware." Output hardware may include, for example, a graphical display terminal, a printer, or a disk drive. See p. 15, lines 22-28 of the specification. As amended, the methods of claims 19 and 21 produce a useful, concrete, and tangible result and are therefore directed to statutory subject matter under Section 101. Applicants therefore request that the Examiner withdraw these rejections.

35 U.S.C. § 112, second paragraph

Claims 23 and 24 stand rejected under Section 112, second paragraph for failing to particularly point out and distinctly claim the subject matter which applicants regard as their invention. The Examiner states that the limitation

"said molecule or molecular complex" in claim 23 lacks antecedent basis, and that the phrase "a set of" is unclear. The Examiner further states that the combination of CnA, CnB, FKBP12, and FK506 residues recited in claim 24 is not commensurate in scope with the specification. Applicants traverse. However, in order to expedite prosecution, applicants have amended claims 23 and 24 to comport with the Examiner's suggestions, thus obviating these rejections.

Specifically, applicants have amended claim 23 to recite "said crystallized molecule or molecular complex," wherein said complex is "defined by the entire set of structure coordinates" as suggested by the Examiner. In addition, applicants have amended claim 24 to recite the molecule or molecular complex comprising "amino acids 17-392 of CnA, amino acids 1-169 of CnB, intact FKBP12 and FK506." This combination is specifically taught in the specification as originally filed, e.g., Example 1, p. 31, lines 4-13. The Examiner has stated that the specification provides support for this particular combination of residues (see the June 20, 2001 Official Action, p. 4), thus obviating these rejections.

Based on the foregoing remarks, applicants request that the Examiner enter the above amendments and allow the claims to pass to issue.

Respectfully submitted,

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APPENDIX

MARKED UP CLAIMS SHOWING AMENDMENTS

19. (Twice Amended) A method for evaluating the ability of a chemical entity to associate with a crystallized molecule or molecular complex comprising a calcineurin A (CnA) binding pocket defined by structure coordinates of CnA amino acids 90, 91, 92, 118, 120, 121, 122, 150, 151, 156, 160, 199, 232, 253, 254, 256, 281, 282, 283, 284, 306, 311, 312, and 317 according to Figure 1, or a homologue of said molecule or molecular complex wherein said homologue comprises a CnA homologue binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å;
wherein said method comprises the steps of:

a. employing computational means to perform a fitting operation between the chemical entity and the CnA binding pocket or the CnA homologue binding pocket; [and]

b. analyzing the results of said fitting operation to quantify the association between the chemical entity and the CnA binding pocket or the CnA homologue binding pocket; and

c. outputting said quantified association to a suitable output hardware.

20. (Twice Amended) [The method according to claim 19, wherein said] A method for evaluating the ability of a chemical entity to associate with a crystallized molecule or molecular complex comprising a CnA binding pocket [is] defined by structure coordinates of CnA amino acids 90, 91, 92, 118, 120, 121, 122, 150, 151, 156, 160, 199, 281, 282,

283, 306, 311, 232, and 254, according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a CnA homologue binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å;

wherein said method comprises the steps of:

a. employing computational means to perform a fitting operation between the chemical entity and the CnA binding pocket or the CnA homologue binding pocket;

b. analyzing the results of said fitting operation to quantify the association between the chemical entity and the CnA binding pocket or the CnA homologue binding pocket; and

c. outputting said quantified association to a suitable output hardware.

21. (Twice Amended) A method for evaluating the ability of a chemical entity to associate with a crystallized molecule or molecular complex comprising a CnA/CnB binding pocket defined by structure coordinates of CnA amino acids 122, 124, 159, 160, 310, 312, 313, 314, 339, 341, 343, 344, 345, 347, 351, 352, 353, 354, 355, 356, 359, 360, and 363; and calcineurin B (CnB) amino acids 49, 50, 114, 115, 118, 119, 121, 122, 123, 124, 157, 158, 159, 161, and 162 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a CnA/CnB homologue binding pocket that has a root mean square deviation from the backbone atoms of said CnA and CnB amino acids of not more than 1.5Å;

wherein said method comprises the steps of:

a. employing computational means to perform a fitting operation between the chemical entity and the

CnA/CnB binding pocket or the CnA/CnB homologue binding pocket; [and]

b. analyzing the results of said fitting operation to quantify the association between the chemical entity and the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket; and

c. outputting said quantified assocation to a suitable output hardware.

22. (Twice Amended) The method according to claim 19 or 20, wherein said crystallized molecule or molecular complex further comprises a second binding pocket defined by CnA amino acids 122, 124, 159, 160, 310, 312, 313, 314, 339, 341, 343, 344, 345, 347, 351, 352, 353, 354, 355, 356, 359, 360, and 363; and CnB amino acids 49, 50, 114, 115, 118, 119, 121, 122, 123, 124, 157, 158, 159, 161, and 162; according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a second homologue binding pocket that has a root mean square deviation from the backbone atoms of said CnA and CnB amino acids of not more than 1.5Å.

23. (Twice Amended) The method according to claim 22, wherein said crystallized molecule or molecular complex is defined by [a] the entire set of structure coordinates according to Figure 1, or a homologue thereof, wherein said homologue has a root mean square deviation from the backbone atoms of said CnA and CnB amino acids of not more than 1.5Å.

24. (Twice Amended) The method according to claim 22, wherein said molecule or molecular complex comprises

amino acids 17-392 of CnA, amino acids 1-169 of CnB, [amino acids 1-107 of] intact FKBP12 and FK506.